

FIGURE 1

rpoB gene of *M. tuberculosis*

Total: 531 bp

tca aggaagaaagc ctacgaactg gcccgcgctcg gtcgctataa (43)
 ggtcaacaag aagctcgggc tgcattgtcg cgagcccatc acgtcgtcga cgctgaccga (103)
 agaagacgtc gtggccacca tgaatatct ggtccgcttg cagcagggtc agaccacgat (163)
 gaccgttcgg ggcggcgctcg aggtgcgggt ggaaccggac gacatcgacc acttcggcaa (223)
 ccgcgccttg cgtacgggtcg tggagctgat ccaaaaccag atccgggctcg gcattctcgg (283)
 gatggagcgg gctgtccggg agcggatgac caccacggac gtggagggga tcaacacgca (343)
 gacgttgatc aacatccggc cgtgtgtcgc cggcatcaag gattcttcgg gcaccaccca (403)
 gctgagccaa ttcattggacc agaacacccc gctgtcgggg ttgacccaca agcgcgcgact (463)
 gtcgggcctg ggcgcgcggc gtctgtctcg tggcgtgc ggtctgggga tccggcgacgt (523)
 ggaacccgt

Underlined letters: Primer binding regions

Bold Letters: polymorphic region existing in *M. tuberculosis* and MOTTs

Italic letters: the region related to the resistance against rifampin

FIGURE 2

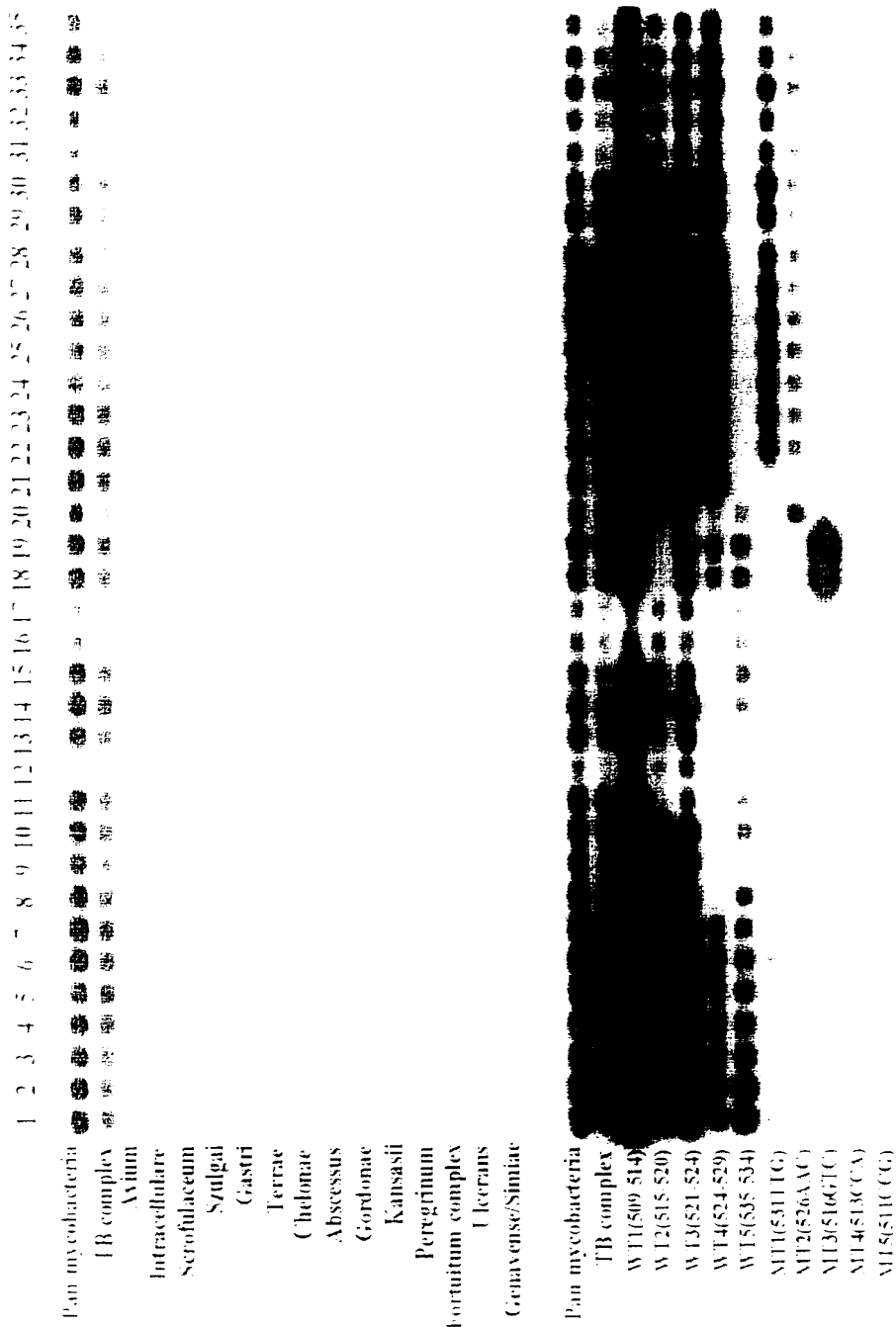


FIGURE 3

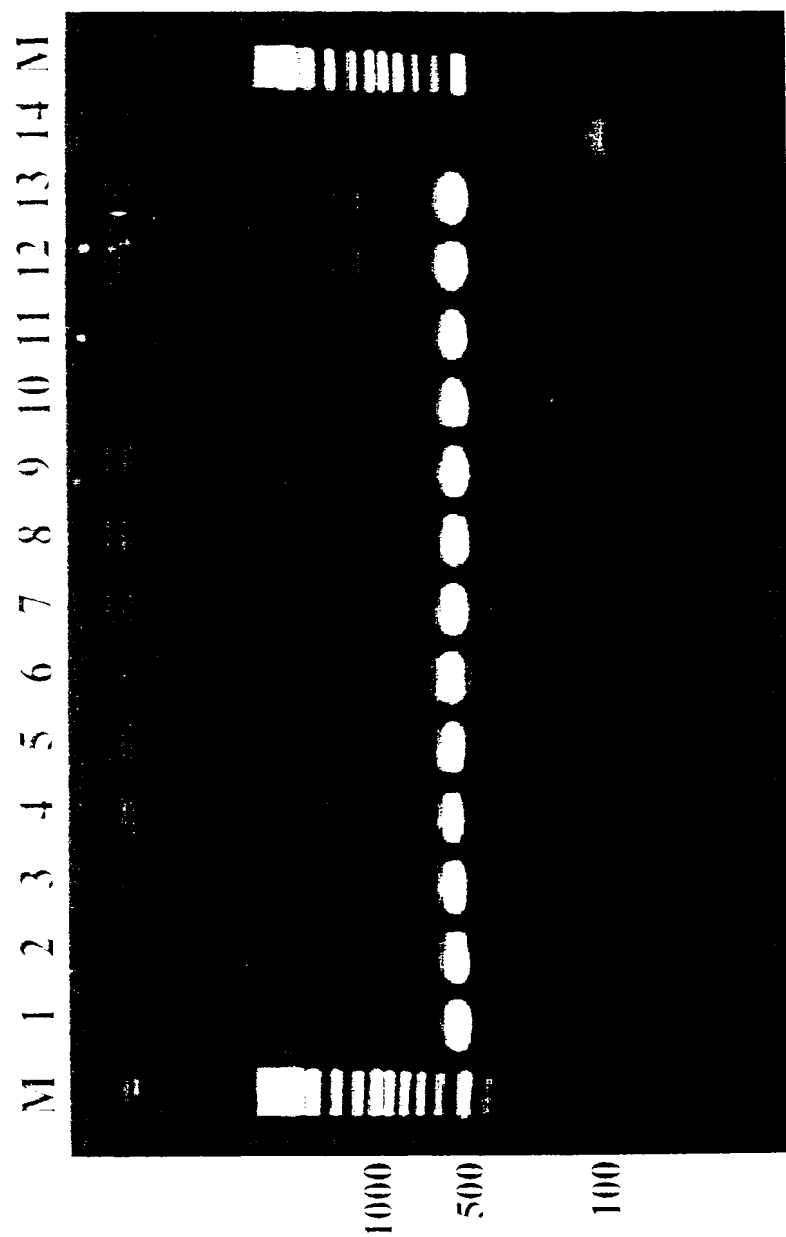


FIGURE 4

M. phylum
M. terminatum
M. caecae
M. triviale
M. tumoresistans
M. phlei
M. parafortuitum
M. flavescens
M. malmoense
M. celatum II
M. celatum I
M. anachromogenicum
M. simiae
M. genavense
M. marinum
M. ulcerans
M. peregrinum
M. fortuitum II
M. fortuitum I
M. kansasii
M. goodii
M. abscessus
M. mageritensis
M. terrae
M. gastri
M. szulgai
M. scrofulaceum
M. intracellulare
M. avium
M. microti
M. africanum
M. bovis BCG
M. bovis
M. tuberculosis H37Rv

Pan-mycobacteria
 TB complex
 Avium
 Intracellular
 Scrofulaceum
 Szulgai
 Gastri
 Terrae
 Chelonae
 Abscessus
 Goodii
 Kansasii
 Peregrinum
 Fortuitum complex
 Ulcerans
 Genavense/Simiae

FIGURE 5

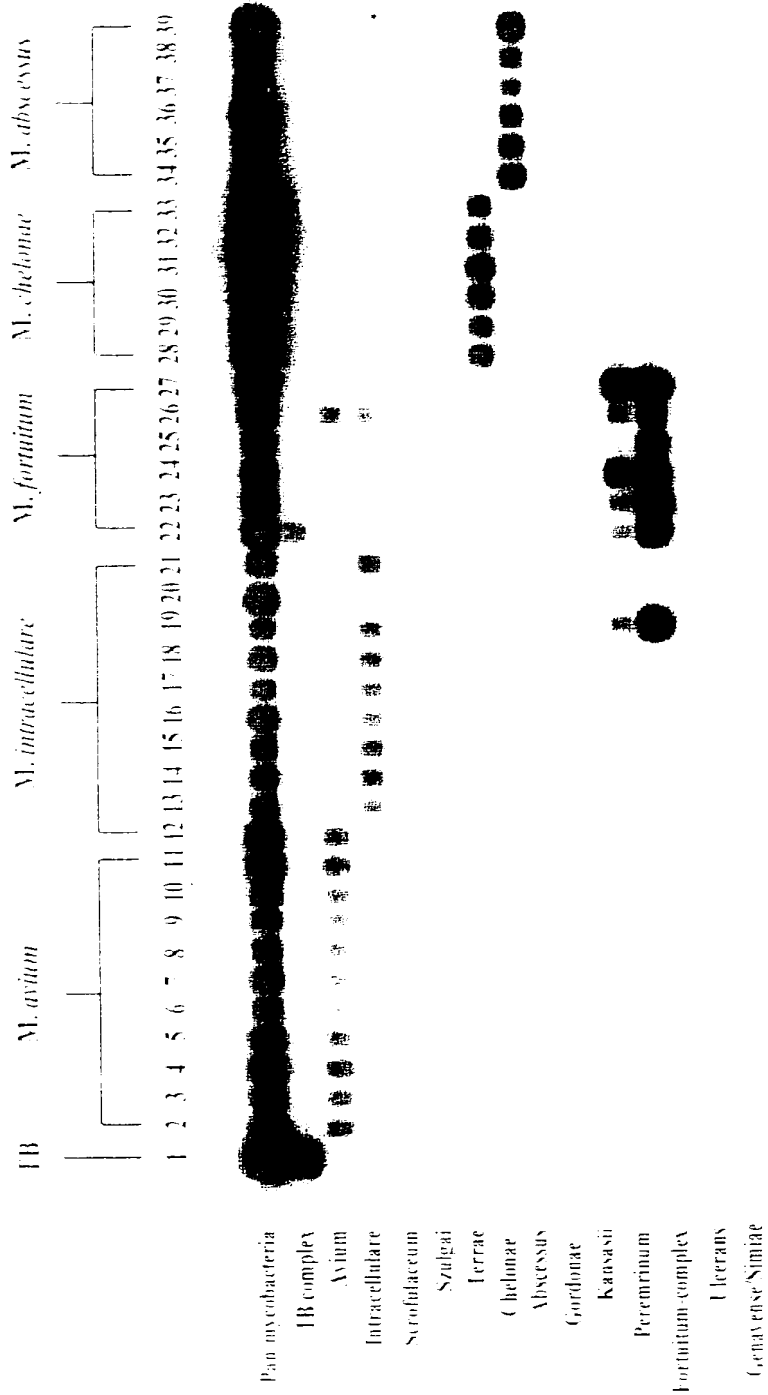


FIGURE 6

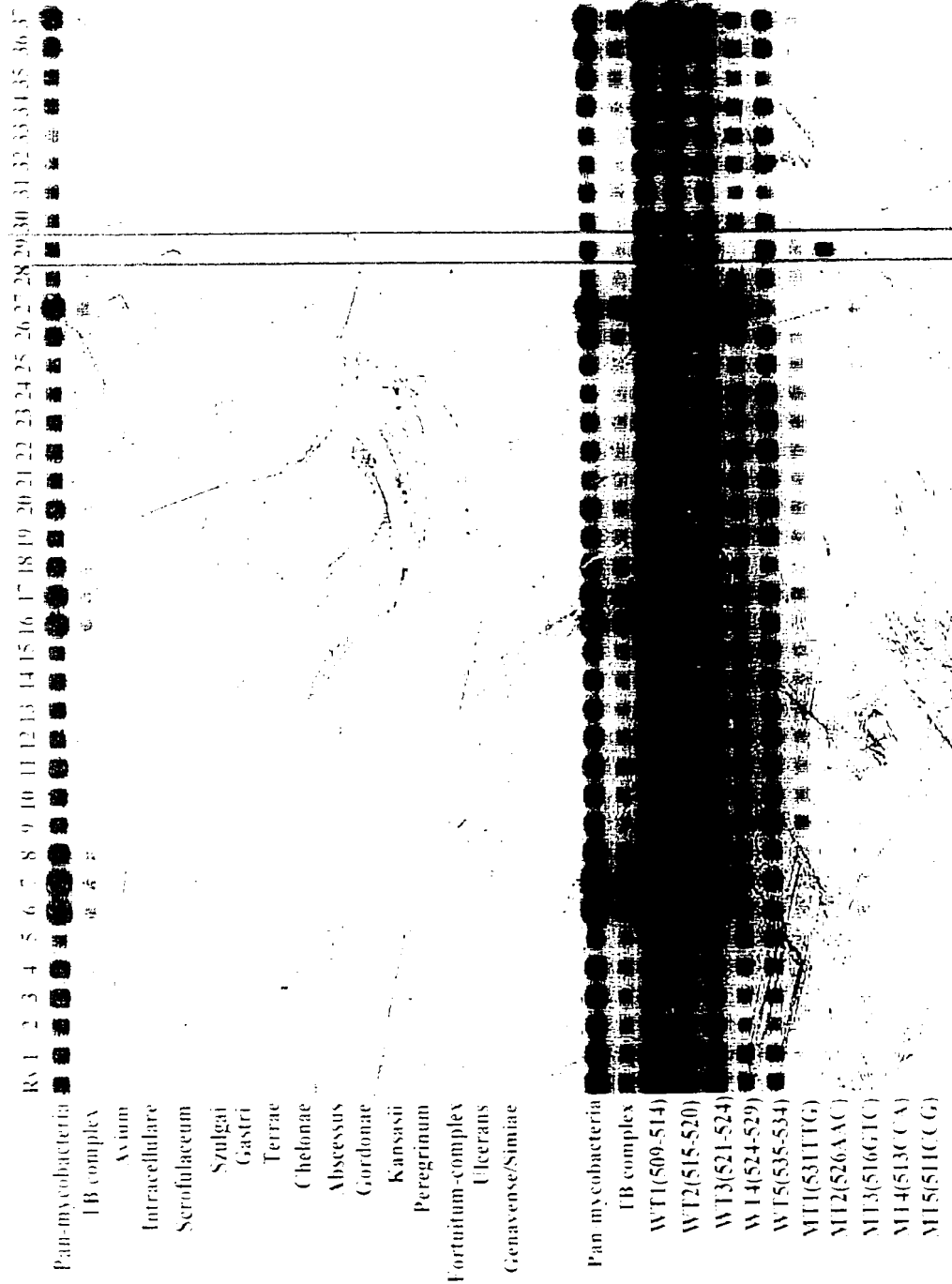


FIGURE 7